

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/836,5440

Source: 1FW/6

Date Processed by STIC: 1/3/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/03/2006

PATENT APPLICATION: US/09/836,544D

TIME: 14:39:37

Input Set : A:\11-88L.ST25.txt

Output Set: N:\CRF4\01032006\I836544D.raw

3 <110> APPLICANT: Seed, Brian
 4 Aruffo, Alejandro
 5 Camerini, David
 7 <120> TITLE OF INVENTION: CD27 Coding Sequence
 9 <130> FILE REFERENCE: 11-88L
 11 <140> CURRENT APPLICATION NUMBER: US 09/836,544D
 12 <141> CURRENT FILING DATE: 2001-04-17
 14 <150> PRIOR APPLICATION NUMBER: US 07/983,647
 15 <151> PRIOR FILING DATE: 1992-12-01
 17 <150> PRIOR APPLICATION NUMBER: US 07/553,759
 18 <151> PRIOR FILING DATE: 1990-07-13
 20 <150> PRIOR APPLICATION NUMBER: US 07/498,809
 21 <151> PRIOR FILING DATE: 1990-03-23
 23 <150> PRIOR APPLICATION NUMBER: US 07/379,076
 24 <151> PRIOR FILING DATE: 1989-07-13
 26 <150> PRIOR APPLICATION NUMBER: US 07/160,416
 27 <151> PRIOR FILING DATE: 1988-02-25
 29 <160> NUMBER OF SEQ ID NOS: 41
 31 <170> SOFTWARE: PatentIn version 3.3
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 2932
 35 <212> TYPE: DNA
 36 <213> ORGANISM: artificial
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: Nucleotide sequence of piH3 vector
 41 <400> SEQUENCE: 1
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 44 gatcaagagc taccaactct ttttccgaag gaactggctt cagcagagcg cagataccaa 120
 46 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcacccg 180
 48 ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc gataagtcgt 240
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 52 cgggggggtc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360
 54 tacagcgtga gctatgagaa agcgccacgc ttcccgaagg gagaaaggcg gacaggtatc 420
 56 cggtaagcgg caggggtcga acaggagagc gcacgagggg gcttcagggg ggaaacgcct 480
 58 ggtatcttta tagtcctgtc gggtttcgcc acctctgact tgagcgctcga tttttgtgat 540
 60 gtcgctcagg ggggcgaggc ctatggaaaa acgccagcaa cgccgaatta ccgcggtggt 600
 62 tctcaacgta acactttaca gcggcgcgctc atttgatatg atgcgccccg cttcccgcata 660
 64 agggagcagg ccagtaaaaag cattaccggt ggtgggggtc ccgagcggcc aaaggagagca 720
 66 gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc cttccccccac caccatcact 780
 68 ttcaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgctg agtagtgccg 840
 70 gagtaaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaactctgt 900
 72 tagggttagg cgttttgcgc tgcttcgcga tgtacggggc agatatacgc gttgacattg 960
 74 attattgact agttattaat agtaatcaat tacgggggtc ttagttcata gcccatatat 1020

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78 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca 1140
80 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgt 1200
82 tcatatgcc agtacgcccc ctattgacgt caatgacggg aaatggcccc cctggcatta 1260
84 tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg tattagtc 1320
86 cgctattacc atggtgatgc ggttttggca gtacatcaat gggcgaggat agcggtttga 1380
88 ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggcacca 1440
90 aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg 1500
92 aattcctggg cgggactggg gagggtggcg ccctcagatg ctgcatataa gcagctgctt 1560
94 tttgcctgta ctgggtctct ctggttagac cagatctgag cctgggagct ctctggctaa 1620
96 ctagagaacc cactgcttaa gcctcaataa agcttctaga gatccctcga cctcgaggga 1680
98 tcttccatac ctaccagttc tgcgcctgca ggtcggcgcc gcgactctag aggatctttg 1740
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104 tttgtgtatt ttagattcca acctatggaa ctgatgaatg ggagcagtggt tggaaatgcct 1920
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108 ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaaggact 2040
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112 gctttgctat ttacaccaca aaggaaaaag ctgactgct atacaagaaa attatggaaa 2160
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130 agtatgcaaa gcatgcatct caattagtca gcaaccaggt gtggaaagtc cccaggtccc 2700
132 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtccccgcc 2760
134 ctaactccgc ccatcccgcc cctaactccg ccaggttccg cccattctcc gccccatggc 2820
136 tgactaattt tttttatttt tgcagaggcc gagggccgct cggcctctga gctattccag 2880
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142 <211> LENGTH: 1504
143 <212> TYPE: DNA
144 <213> ORGANISM: Homo sapiens
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (7)..(1059)
151 <400> SEQUENCE: 2
152 cctaag atg agc ttt cca tgt aaa ttt gta gcc agc ttc ctt ctg att 48
153 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile
154 1 5 10
156 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
157 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
158 15 20 25 30
160 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
161 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
162 35 40 45

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164	agt	ttt	caa	atg	agt	gat	gat	att	gac	gat	ata	aaa	tgg	gaa	aaa	act	192
165	Ser	Phe	Gln	Met	Ser	Asp	Asp	Ile	Asp	Asp	Ile	Lys	Trp	Glu	Lys	Thr	
166			50					55					60				
168	tca	gac	aag	aaa	aag	att	gca	caa	ttc	aga	aaa	gag	aaa	gag	act	ttc	240
169	Ser	Asp	Lys	Lys	Lys	Ile	Ala	Gln	Phe	Arg	Lys	Glu	Lys	Glu	Thr	Phe	
170			65				70					75					
172	aag	gaa	aaa	gat	aca	tat	aag	cta	ttt	aaa	aat	gga	act	ctg	aaa	att	288
173	Lys	Glu	Lys	Asp	Thr	Tyr	Lys	Leu	Phe	Lys	Asn	Gly	Thr	Leu	Lys	Ile	
174			80				85					90					
176	aag	cat	ctg	aag	acc	gat	gat	cag	gat	atc	tac	aag	gta	tca	ata	tat	336
177	Lys	His	Leu	Lys	Thr	Asp	Asp	Gln	Asp	Ile	Tyr	Lys	Val	Ser	Ile	Tyr	
178	95					100					105					110	
180	gat	aca	aaa	gga	aaa	aat	gtg	ttg	gaa	aaa	ata	ttt	gat	ttg	aag	att	384
181	Asp	Thr	Lys	Gly	Lys	Asn	Val	Leu	Glu	Lys	Ile	Phe	Asp	Leu	Lys	Ile	
182				115						120					125		
184	caa	gag	agg	gtc	tca	aaa	cca	aag	atc	tcc	tgg	act	tgt	atc	aac	aca	432
185	Gln	Glu	Arg	Val	Ser	Lys	Pro	Lys	Ile	Ser	Trp	Thr	Cys	Ile	Asn	Thr	
186				130					135					140			
188	acc	ctg	acc	tgt	gag	gta	atg	aat	gga	act	gac	ccc	gaa	tta	aac	ctg	480
189	Thr	Leu	Thr	Cys	Glu	Val	Met	Asn	Gly	Thr	Asp	Pro	Glu	Leu	Asn	Leu	
190			145					150					155				
192	tat	caa	gat	ggg	aaa	cat	cta	aaa	ctt	tct	cag	agg	gtc	atc	aca	cac	528
193	Tyr	Gln	Asp	Gly	Lys	His	Leu	Lys	Leu	Ser	Gln	Arg	Val	Ile	Thr	His	
194			160				165					170					
196	aag	tgg	acc	acc	agc	ctg	agt	gca	aaa	ttc	aag	tgc	aca	gca	ggg	aac	576
197	Lys	Trp	Thr	Thr	Ser	Leu	Ser	Ala	Lys	Phe	Lys	Cys	Thr	Ala	Gly	Asn	
198	175					180					185				190		
200	aaa	gtc	agc	aag	gaa	tcc	agt	gtc	gag	cct	gtc	agc	tgt	cca	gag	aaa	624
201	Lys	Val	Ser	Lys	Glu	Ser	Ser	Val	Glu	Pro	Val	Ser	Cys	Pro	Glu	Lys	
202				195						200					205		
204	ggg	ctg	gac	atc	tat	ctc	atc	att	ggc	ata	tgt	gga	gga	ggc	agc	ctc	672
205	Gly	Leu	Asp	Ile	Tyr	Leu	Ile	Ile	Gly	Ile	Cys	Gly	Gly	Gly	Ser	Leu	
206				210					215					220			
208	ttg	atg	gtc	ttt	gtg	gca	ctg	ctc	gtt	ttc	tat	atc	acc	aaa	agg	aaa	720
209	Leu	Met	Val	Phe	Val	Ala	Leu	Leu	Val	Phe	Tyr	Ile	Thr	Lys	Arg	Lys	
210			225					230					235				
212	aaa	cag	agg	agt	cgg	aga	aat	gat	gag	gag	ctg	gag	aca	aga	gcc	cac	768
213	Lys	Gln	Arg	Ser	Arg	Arg	Asn	Asp	Glu	Glu	Leu	Glu	Thr	Arg	Ala	His	
214			240				245					250					
216	aga	gta	gct	act	gaa	gaa	agg	ggc	cgg	aag	ccc	cac	caa	att	cca	gct	816
217	Arg	Val	Ala	Thr	Glu	Glu	Arg	Gly	Arg	Lys	Pro	His	Gln	Ile	Pro	Ala	
218	255					260					265				270		
220	tca	acc	cct	cag	aat	cca	gca	act	tcc	caa	cat	cct	cct	cca	cca	cct	864
221	Ser	Thr	Pro	Gln	Asn	Pro	Ala	Thr	Ser	Gln	His	Pro	Pro	Pro	Pro	Pro	
222				275						280					285		
224	ggg	cat	cgt	tcc	cag	gca	cct	agt	cat	cgt	ccc	ccg	cct	cct	gga	cac	912
225	Gly	His	Arg	Ser	Gln	Ala	Pro	Ser	His	Arg	Pro	Pro	Pro	Pro	Gly	His	
226				290						295					300		
228	cgt	gtt	cag	cac	cag	cct	cag	aag	agg	cct	cct	gct	ccg	tcg	ggc	aca	960

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233 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
234          320          325          330
236 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct      1056
237 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
238 335          340          345          350
240 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg      1109
241 Asn
244 cctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca      1169
246 cctcctgagg ctgtgggccca cagccacctc tgcattctcg aactcagcca tgtgggtcaac      1229
248 atctggagtt tttggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa      1289
250 gtgtgattgc aagaatggta gaggaccgag cacagaaaac ttagagattt cttgtcccct      1349
252 ctcaggatcat gtgtagatgc gataaatcaa gtgattgggtg tgcctgggtc tcactacaag      1409
254 cagcctatct gcttaagaga ctctggagtt tcttatgtgc cctggtggac acttgccac      1469
256 catcctgtga gtaaaaagtga aataaaaagct ttgac      1504
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260 <211> LENGTH: 351
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
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271          20          25          30
274 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
275          35          40          45
278 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
279          50          55          60
282 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
283 65          70          75          80
286 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
287          85          90          95
290 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
291          100          105          110
294 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
295          115          120          125
298 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
299          130          135          140
302 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
303 145          150          155          160
306 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
307          165          170          175
310 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
311          180          185          190
314 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
315          195          200          205
318 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met

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319      210      215      220
322 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
323 225      230      235      240
326 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
327      245      250      255
330 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
331      260      265      270
334 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
335      275      280      285
338 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
339      290      295      300
342 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
343 305      310      315      320
346 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
347      325      330      335
350 Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
351      340      345      350
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355 <211> LENGTH: 874
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
360 <220> FEATURE:
361 <221> NAME/KEY: CDS
362 <222> LOCATION: (13)..(723)
364 <400> SEQUENCE: 4
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366      Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val
367      1      5      10
369 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt      99
370 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
371      15      20      25
373 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta      147
374 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
375 30      35      40      45
377 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat      195
378 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
379      50      55      60
381 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt      243
382 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
383      65      70      75
385 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac      291
386 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
387      80      85      90
389 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat      339
390 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
391      95      100      105
393 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca      387
394 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
395 110      115      120      125

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/836,544D

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:38; Xaa Pos. 1,4

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,6,37,38

VERIFICATION SUMMARY

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Input Set : A:\11-88L.ST25.txt

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L:3794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0